IN THE CLAIMS:

Applicants, pursuant to 37 C.F.R. § 1.121, submit the following amendments to the claims:

1. (Currently Amended) A method for the analysis of breast cell proliferative disorders, comprising determining ~~by determination of~~ the genomic methylation status of at least one CpG dinucleotide of at least one sequence selected ~~state of one or more sequences~~ from the sequence group consisting of SEQ ID NOS:1-73, SEQ ID NO:366, contiguous portions thereof, and sequences complementary thereto ~~Seq. ID No.1 through Seq. ID No. 73 and Seq. ID No. 366~~.

2. (Currently Amended) The ~~A~~ method of ~~according to~~ Claim 1, ~~said method comprising~~ wherein determining the genomic methylation status of the at least one CpG dinucleotide, comprises: obtaining a biological sample comprising genomic DNA from a subject; and contacting the genomic DNA ~~a nucleic acid consisting essentially of one or more sequences from the group of Seq. ID No. 1 through Seq. ID No. 73 and Seq. ID No. 366 in a biological sample obtained from a subject~~ with at least one reagent, or a series of reagents, which ~~wherein said reagent or series of reagents,~~ distinguishes between methylated and non-methylated ~~non-methylated~~ CpG dinucleotides ~~within the target nucleic acid(s) from the group of Seq. ID No.1 through Seq. ID No. 73 and Seq. ID No. 366~~.

3. (Currently amended) A nucleic acid molecule consisting essentially of a sequence at least 18 contiguous bases in length of a sequence selected ~~according to one of the sequences taken~~ from the sequence group consisting of SEQ ID NOS:74-365, and SEQ ID NOS:367-370, ~~comprising Seq. ID No. 74 through Seq. ID No. 365 and Seq. ID No. 367 through Seq. ID No. 370~~ and sequences complementary thereto.

4. (Currently amended) An oligomer, ~~in particular an oligonucleotide or peptide nucleic acid (PNA) oligomer, said oligomer~~ consisting essentially of a ~~essentially of at least one base~~ sequence ~~having a length~~ of at least 10 contiguous nucleotides in length that ~~which~~ hybridises to or is identical to a sequence selected from the group consisting of SEQ ID NOS:1-370 ~~one of the nucleic acid sequences according to Seq. ID No. 1 through Seq. ID No. 370~~.

5. (Currently amended) The oligomer of ~~as recited in~~ Claim 4, wherein the contiguous base sequence includes at least one CpG dinucleotide.

6. (Currently amended) The oligomer of ~~as recited in~~ Claim 5, wherein ~~characterised in that~~ the cytosine of the CpG dinucleotide is located in about the middle third of the oligomer.

7. (Original) A set of oligomers, comprising at least two oligomers according to any of claims 4 to 6.

8. (Currently amended) The ~~A~~ set of oligomers of ~~as recited in~~ Claim 7, comprising oligomers for detecting the methylation state of all CpG dinucleotides within sequences of the sequence group consisting of SEQ ID NOS:1-73, SEQ ID NO: 366, contiguous portions thereof, ~~Seq. ID No.1 through Seq. ID No. 73 and Seq. ID No. 366~~ and sequences complementary thereto.

9. (Currently amended) The ~~A~~ set of oligomers of Claim 7, wherein the set is suitable for use ~~at least two oligonucleotides as recited in one of Claims 4 through 8, which is used~~ as primer oligonucleotides for the amplification of a sequence selected from the sequence group consisting ~~nucleic acid sequences of one~~ of SEQ ID NOS:1-370, contiguous portions thereof, ~~Seq. ID No. 1 through Seq. ID No. 370~~ and sequences complementary thereto.

10. (Currently amended) The ~~A~~ set of oligomers according to any ~~oligonucleotides as recited in~~ one of Claims 7 through 9, wherein ~~characterised in that~~ at least one oligomer ~~oligonucleotide~~ is bound to a solid phase.

11. (Currently amended) A method for determining methylation state or for detecting single nucleotide polymorphisms, comprising using ~~Use of~~ a set of oligonucleotides comprising at least three ~~of the~~ oligomers according to any of claims 4 through 10 in an assay suitable for at least one of detecting ~~the~~ cytosine methylation state and ~~and/or~~ single nucleotide polymorphisms (SNPs), within a sequence selected from the group consisting of SEQ ID NOS:1-370, contiguous portions thereof, ~~the sequences taken from the group of Seq. ID No. 1 to Seq. ID No. 370~~ and sequences complementary thereto.

12. (Currently amended) A method for manufacturing an arrangement of different oligomers (array) fixed to a carrier material and suitable for analysing breast cell proliferative disorders associated with the methylation state of ~~any~~ of at least one CpG dinucleotide of a sequence selected from the group consisting of SEQ ID NOS:1-73 and SEQ ID NO:366, contiguous portions thereof, and sequences complementary thereto, comprising coupling ~~the CpG dinucleotides of the group Seq. ID No.1 through Seq. ID No. 73 and Seq. ID No. 366, wherein~~ at least one nucleic acid or oligomer according to any of the claims 3 through 10 ~~is coupled~~ to a solid phase.

13. (Currently amended) An arrangement of different oligomers (array) obtainable according to ~~the method of~~ claim 12.

14. (Currently amended) The arrangement of Claim 13, wherein the oligomers are at least one of oligonucleotides and ~~An array of different oligonucleotide- and/or~~ PNA-oligomer sequences ~~as recited in Claim 13~~, wherein the carrier material is a planar ~~characterised in that these are arranged on a plane~~ solid phase, and wherein the oligomers are arranged thereon in the form of a rectangular or hexagonal lattice.

15. (Currently amended) The arrangement of Claim 13, wherein the carrier material comprises a material selected from the group consisting of ~~array as recited in any of the Claims 13 or 14, characterised in that the solid phase surface is composed of~~ silicon, glass, polystyrene, aluminium, steel, iron, copper, nickel, silver, ~~or~~ gold, and combinations thereof.

16. (Currently amended) An oligomer array suitable ~~A DNA- and/or PNA-array~~ for analysing breast cell proliferative disorders associated with the methylation state of at least one CpG dinucleotide of a sequence selected from the group consisting of SEQ ID NOS:1-73, SEQ ID NO:366, contiguous portions thereof, and sequences complementary thereto, ~~any of the CpG dinucleotides of the group Seq. ID No.1 through Seq. ID No. 73 and Seq. ID No.366~~ the array comprising at least one nucleic acid or oligomer according to any one of ~~the preceding~~ claims 3 through 10.

17. (Currently amended) A method for the analysis of breast cell proliferative disorders, comprising ~~according to Claim 1 or 2 characterised in that the following steps are carried out~~:

a) obtaining a biological sample comprising genomic DNA;

b) ~~a)~~ contacting the ~~in a~~ genomic DNA ~~sample~~, or a portion thereof with an agent or combination of agents suitable to convert cytosine bases that ~~which~~ are unmethylated at the 5-position ~~are converted, by chemical treatment,~~ to uracil or to another base which is dissimilar to cytosine in terms of hybridisation behaviour, to provide a pretreated DNA;

c) ~~b)~~ amplifying, using at least one set of primer oligonucleotides and a polymerase, at least one pretreated DNA sequence, ~~fragment~~ or a portion thereof, selected from the sequence group consisting of SEQ ID NOS:74-365, SEQ ID NOS:367-370, contiguous portions thereof, ~~of the pretreated genomic DNA using sets of primer oligonucleotides and a polymerase, wherein said fragments comprise one or more sequences taken from the group of Seq. ID No. 74 to Seq. ID No. 365 and SEQ ID NO: 367 to SEQ ID NO: 370~~ and sequences complementary thereto;

d) ~~c)~~ determining, based on the amplification, or on analysis of the nucleic acid amplificate, the methylation status of one or more ~~the~~ genomic CpG dinucleotides ~~by analysis of the amplificate nucleic acids~~, whereby analysis of breast cell proliferative disorders is, at least in part, afforded.

18. (Currently amended) The method of ~~as recited in~~ Claim 17, wherein determining in d) comprises ~~characterised in that Step c) is carried out by means of~~ hybridisation of at least one nucleic acid or oligomer ~~oligonucleotide~~ according to any one of Claims 3 through 10.

19. (Currently amended) The method of ~~as recited in~~ Claim 17, wherein determining in d) comprises ~~characterised in that Step c) is carried out by means of~~ hybridisation of at least one oligonucleotide according to any one of Claims 3 through 10, and extension of the at least one ~~said~~ hybridised oligonucleotide~~(s)~~ by ~~means of~~ at least one nucleotide base.

20. (Currently amended) The method of ~~as recited in~~ Claim 17, wherein determining in d) comprises ~~characterised in that Step c) is carried out by means of~~ sequencing.

21. (Currently amended) The method of ~~as recited in~~ Claim 17, wherein amplifying in c) comprises

~~characterised in that Step b) is carried out~~ using methylation-specific ~~methylation-specific~~ primers.

22. (Currently amended) The method of ~~as recited in~~ Claim 17, wherein determining in d) comprises use ~~characterised in that Step c) is carried out by means~~ of a combination of at least two of the methods described in any one of Claims 18 through 21.

23. (Currently amended) The method of ~~as recited in~~ Claim 17, wherein contacting in c) comprises contacting with at least one agent selected from the group consisting of ~~characterised in that the chemical treatment is carried out by means of a solution of a~~ bisulfite, hydrogen sulfite or disulfite.

24. (Currently amended) A method for the analysis of breast cell proliferative disorders, comprising ~~according to Claims 1 and 2 characterised in that the following steps are carried out~~:

a) obtaining, from a subject, a biological sample containing genomic DNA;~~,~~

b) isolating ~~extracting~~ the genomic DNA;~~,~~

c) digesting the isolated genomic DNA, or a portion thereof comprising at least one ~~or more of the sequences~~ sequence selected from the sequence group consisting of SEQ ID NOS1-73, SEQ ID NO:366, contiguous portions thereof, and sequences complementary thereto, ~~comprising Seq. ID No. 1 through Seq. ID No. 73 and Seq. ID No. 366~~ with one or more methylation-sensitive methylation sensitive restriction enzymes;~~,~~ and

d) detecting ~~detection of~~ the DNA fragments generated in ~~the digest of step~~ c), whereby analysis of breast cell proliferative disorders is, at least in part, afforded.

25. (Currently amended) The ~~A~~ method of ~~according to~~ Claim 24, further comprising, prior to d), amplifying ~~wherein~~ the DNA digest ~~is amplified prior to Step d)~~.

26. (Currently amended) The method of any ~~as recited in~~ one of ~~the~~ Claims 17 ~~through 23~~ and 25, wherein ~~characterised in that~~ more than ten different fragments having a length of about 100 to about 200 ~~100 – 200~~ base pairs are amplified.

27. (Currently amended) The method of any ~~as recited in~~ one of Claims 17 ~~through 23, 25~~ and 26, wherein ~~characterised in that the~~ amplification of several DNA segments is carried out in one reaction vessel.

28. (Currently amended) The method of any ~~as recited in~~ one of ~~the~~ Claims 17 ~~through 23~~ and 25, wherein amplifying is by means of ~~through 27, characterised in that the polymerase is~~ a heat-resistant DNA polymerase.

29. (Currently amended) The method of any ~~as recited in~~ one of ~~the~~ Claims 17 ~~through 23~~ and 25, wherein amplifying is by means of a ~~through 28, characterised in that the amplification is carried out by means of the~~ polymerase chain reaction (PCR).

30. (Currently amended) The method of any ~~as recited in~~ one of ~~the~~ Claims 17 ~~through 23~~ and 25, wherein ~~through 29, characterised in that~~ the amplificates carry detectable labels.

31. (Currently amended) The method of ~~according to~~ Claim 30, wherein said labels are selected from the group consisting of fluorescence labels, radionuclides, ~~and/or~~ detachable molecule fragments having a typical mass which can be detected in a mass spectrometer, and combinations thereof.

32. (Currently amended) The method of Claim 17, wherein ~~as recited in one of the Claims 17 through 23, characterised in that the~~ amplificates or fragments of the amplificates are detected in the mass spectrometer.

33. (Currently amended) The method of any ~~as recited in~~ one of ~~the~~ Claims 31 and ~~and/or~~ 32, wherein ~~characterised in that the~~ produced fragments have a single positive or negative net charge for better detectability in the mass spectrometer.

34. (Currently amended) The method of Claim 30, wherein ~~as recited in one of Claims 30 through 33, characterised in that~~ detection is carried out and visualised by means of at least one of matrix assisted laser desorption/ionisation mass spectrometry (MALDI), and ~~or~~ using electron spray

mass spectrometry (ESI).

35. (Currently amended) The method of any ~~as recited in~~ one of ~~the~~ Claims 17 and 24, wherein ~~through 30, characterised in that~~ the genomic DNA is obtained from cells or cellular components which contain DNA, sources of DNA comprising, for example, cell lines, histological slides, biopsies, tissue embedded in paraffin and all possible combinations thereof.

36. (Currently amended) A kit reagent having at least one of bisulfite, disulfite, and hydrogen sulfite, ~~bisulfite (= disulfite, hydrogen sulfite) reagent~~ as well as at least one of oligonucleotides, and ~~and/or~~ PNA-oligomers according to any one of the Claims 4 through 10.

37. (Currently amended) The ~~A~~ kit of ~~according to~~ claim 36, further comprising standard reagents for performing a methylation assay selected from the group consisting of MS-SNuPE, MSP, MethyLight~~Methyl light~~, HeavyMethyl~~Heavy Methyl~~, nucleic acid sequencing, and combinations thereof.

38. (Cancelled ) ~~The use of a method according to one of claims 1, 2, 12, and 17 to 35, a nucleic acid according to Claim 3, of an oligonucleotide or PNA-oligomer according to one of the Claims 4 through 10, of a kit according to Claim 36 or 37, of an array according to one of the Claims 14 through 16 or of a set of oligonucleotides according to one of claims 7 through 10 for the characterisation, classification, differentiation, grading, staging, and/or diagnosis of breast cell proliferative disorders, or the predisposition to cell proliferative disorders~~.

39. (Cancelled) ~~The use of a method according to one of claims 1, 2, 12, and 17 to 35, a nucleic acid according to Claim 3, of an oligonucleotide or PNA-oligomer according to one of the Claims 4 through 10, of a kit according to Claim 36 or 37, of an array according to one of the Claims 14 through 16 or of a set of oligonucleotides according to one of claims 7 through 10 for the therapy of breast cell proliferative disorders~~.

40. (New) The oligomer of claim 4, wherein the oligomer is an oligonucleotide or a peptide nucleic acid (PNA)-oligomer.